ETHICS & INNOVATION Balancing Large Language Models in the Research Ecosystem

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this break-out session has been generated with the help of chatGPT 4 and 40

Introduction

- Welcome and brief overview of break-out session objectives
- Importance of ethics in research
- Introduction to Large Language Models (LLMs) and their significance in life sciences



2022



Message ChatGPT



Google is a librarian GPT is the one who read all the books

How LLMs work

after pre-training



Total: -0.96 logprob on 1 token (73.18% probability covered in top 5 logits)

Q & A in natural language



Q & A session



Q & A + additional knowledge



API access



Al modules



Al modules



Applications of LLMs in Research Supporting data analysis

- Language guided analysis
- Generate code for scripted data analyses (reproducible!)
- Support coding
- Providing access to complex methods
- Assist results interpretation
- Generating insights and hypotheses

DG 16 Glucose IVGTTs

Unable to display visualization

in the table there are time course measurements of glucose levels in animals that differ in genotype ("Genetik"), diet ("IVGTT") and sex ("Geschlecht"). The column name of time course measurements indicate time in hours (-10 up to 150).

Please suggest and perform an analysis that shows if there is a difference in kinetics depending on genotype and/or diet

Analyzed



Analyzed

pythen	Always show details 🌔 🗗 Copy code
<pre>a Load the data from the sheet df = pd.read_excel[file_path, sheet_name="01</pre>	.c mmcl-L')
# Display the first few rows to uncerstand i df.head()	ts structure
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1 11762 DG2 GIPRdn-LCMP GIPRdn	w Basis 3.9 4.0 21.1 17
2 11763 CG2 GIPRdn-LCMP GIPRdn	w Besis 4.1 3.9 17.8 13
3 11609 DO1 0IPRdn-LCMP GIPRdn	w Basis 4.9 4.9 19.6 16
4 11610 DG1 GIPRdn-LCMP GIPRdn	w Basis 4.1 3.9 21.5 18
22 30 40 50 60 🕡 100	110 129 150
8 8.3 6.8 4.8 3.9 3.4 3.4 3.4	3.5 3.5 3.7

ChatGPT 4o ~





Step 4: Statistical Testing

We'll use two-way ANOVA to test the effects of genotype and diet on glucose levels over time. This will help us understand if either factor or their interaction significantly impacts glucose kinetics.

Let's perform the ANOVA test. [--]

Analyzed



ANOVA Results Interpretation

- 1. Genotype: The p-value for genotype (p = 0.054877) is slightly above the typical threshold of 0.05, suggesting that the effect of genotype on glucose levels is not statistically significant at the 5% level.
- Diet (IVGTT): The p-value for diet (p = 0.000330) is well below 0.05, indicating a significant effect of diet on glucose levels.
- 3. Interaction (Genotype

): The p-value for the interaction between genotype and diet (p=0.952529) is very high, suggesting no significant interaction effect.

Conclusion

- Diet has a significant impact on glucose kinetics.
- · Genotype does not have a statistically significant effect.
- · There is no significant interaction between genotype and diet.

If you need further analysis or specific visualizations, please let me know! [>-]



I have a table called 'glucose.csv'. How do I analyse it - summary statistics, tests, visualisation - using R?



Certainly! Analyzing a CSV file in R involves a few steps. Let's walk through the process of analyzing your 'glucose.csv' data. Here's a comprehensive guideline:

1. Loading Necessary Libraries

First, you need to have the necessary libraries. Install them if you haven't:

R				🗂 Copy code
<pre>install.packages(c("tidyverse",</pre>	"ggplot2",	"dplyr",	"readr",	"summarytools"

Now, load them:

R	Copy code
library(tidyverse)	
library(summarytools)	
library(lubridate)	

2. Reading the Data



3. Basic Examination of the Data

> head(glucose_data)

A tibble: 6 × 28

...1 Animal DG Expt_Group Genotype Sex IVGTT `-10` `0` `1` `3` `5` `7` `10` `15` `20` `30` `40` `50` `60` `90` `100` `110` `120` `150` Timpoint Diet AUC

<dbl> <chr> <chr> <chr> <chr> <chr> <chr> <dbl> <dbl > <dbl >

1 1 Tier_11765 DG2 GIPRdn-CONTROL GIPRdn w Basis 3.8 3.6 18.4 16.2 15.1 12.9 11.6 9.8 8.3 6.8 4.8 3.9 3.4 3.4 3.4 3.5 3.5 3.7 Basis CONTROL 804.

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3 3 Tier_11763 DG2 GIPRdn-LCMP GIPRdn w Basis 4.1 3.9 17.8 13.9 13.5 12.8 11.8 10.7 9.8 8.7 7.6 6.8 6 4.5 4.1 4.2 4.2 4.2 Basis LCMP 1001.

4 4 Tier_11609 DG1 GIPRdn-LCMP GIPRdn w Basis 4.9 4.9 19.6 16.2 15.6 14.1 12.6 10.9 10.4 8.5 6.9 5.4 4.7 3.8 NA NA NA NA Basis LCMP 722.

TS

Thank you for sharing a snippet of your dataset. Here's a more detailed approach to analyzing this particular structure:

1. Examine the Dataset's Attributes

From the given snippet, I see a repeated measure design. The glucose levels are measured at different time points ('-10', '0', '1', '3', and so forth). You have categorical variables such as 'Animal', 'Expt_Group', 'Genotype', 'Sex', 'IVGTT', 'Timpoint', and 'Diet'. The numeric columns include the aforementioned time points and 'AUC'.

1. Summary Statistics

ß

For categorical columns:

R			Ć	Copy code
<pre>lapply(glucose_data[, c("Expt_Group",</pre>	"Genotype",	"Sex",	"IVGTT",	"Timpoint"

For numeric columns (excluding the first column which seems to be an ID column):



1. Visualizations

Boxplots grouped by experiment group for a specific time point:



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Applications of LLMs in Research Manuscript writing

- Drafting / structuring content
- Improving language and clarity
- Generating abstracts and summaries

ChatGPT 40 ~

): The p-value for the interaction between genotype and diet (p = 0.952529) is very high, suggesting no significant interaction effect.

Conclusion

- Diet has a significant impact on glucose kinetics.
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- There is no significant interaction between genotype and diet.

If you need further analysis or specific visualizations, please let me know! [-]

0) D Q &~

Based on this findings please draft a manuscript for publication

(Ittle: The Impact of Diet on Glucose Kinetics in Different Genotypes

Abstract

This study investigates the effect of genotype and diet on glucose kinetics in a controlled animal model. Using a time-course measurement of glucose levels, we aimed to determine whether these factors significantly influence glucose metabolism. Our results indicate that diet significantly impacts glucose levels over time, while genotype does not show a statistically significant effect. Additionally, no significant interaction between genotype and diet was observed. These findings highlight the importance of dietary factors in regulating glucose metabolism, providing insights for future research in metabolic health.

Introduction

Glucose metabolism is a critical aspect of metabolic health, influenced by various genetic and environmental factors. Understanding how these factors interact can provide insights into the mechanisms underlying metabolic disorders such as diabetes. Previous studies have shown that both genotype and diet play essential roles in glucose regulation. However, the relative contributions of these factors and their interaction effects remain unclear. This study aims to elucidate the impact of genotype and diet on glucose kinetics using a controlled animal model, providing a comprehensive analysis of their effects over time.

Methods

Animals and Experimental Design

The study involved multiple animal subjects differing in genotype, diet, and sex. The animals were divided into groups based on their genotype (GIPRdn) and diet (CONTROL, LCMP, etc.). Each group's glucose levels were measured at multiple time points, ranging from -10 to 150 hours, using standard intravenous glucose tolerance tests (IVGTT).

Data Collection

Glucose measurements were recorded at specified time intervals, resulting in a time-course dataset. The primary variables of interest where details and plucose levels at each time.

Applications of LLMs in Research

Grant application drafting

- Assistance in proposal writing
- Enhancing persuasive language
- Formatting and compliance checks

Applications of LLMs in Research

Conducting literature reviews

- Summarizing existing research
- Identifying key studies and gaps

ChatGPT 40 \



please highlight the shortcomings of this study

- Here are some potential shortcomings of the study "Neuronal Hyperactivity in Neurons Derived from Individuals with Grey Matter Heterotopia":
 - Model Limitations: The study relies heavily on human cerebral organoids (hCOs) to model periventricular heterotopia (PH). While hCOs are valuable tools, they cannot fully replicate the complexity and cellular diversity of the human brain. The results from hCOs might not translate perfectly to in vivo human conditions.
 - Genetic Heterogeneity: The study examines neurons derived from patients with specific mutations in FAT4 or DCHS1. However, PH can be caused by mutations in several other genes, and the study's findings might not be generalizable to all forms of PH.
 - Sample Size and Variability: The sample size in the study, particularly the number of independent hCOs and neurons analyzed, might be limited. Small sample sizes can reduce the statistical power and increase the variability of the results.
 - 4. Single-cell Analysis: While the study uses advanced techniques like patch-clamp recordings and silicon probe recordings, single-cell transcriptome and proteome analyses might have provided more detailed insights into the cellular heterogeneity and specific neuronal subtypes affected in PH.
 - Temporal Dynamics: The study focuses on 9-month-old hCOs, which might not capture the entire developmental trajectory and dynamic changes occurring in neurons over time. Observing changes at multiple developmental stages could provide a more comprehensive understanding.
 - In Vivo Validation: The findings from hCOs would benefit from in vivo validation in animal models or human tissues to confirm the relevance of the observed neuronal hyperactivity and molecular alterations in a more complex and integrated biological system.
 - 7. Functional Consequences: While the study demonstrates hyperactivity and morphological changes in neurons, the functional consequences of these alterations on neural network behavior and cognitive functions remain unclear. Behavioral studies or more complex network analyses could shed light on this aspect.
 - 8. Technical Variability: The use of different techniques, such as silicon probe recordings and patch-clamp recordings, might introdu technical variability. Consistency and

Applications of LLMs in Research Interaction with knowledge

- Question answer sessions with model or prompt-based knowledge
- Further training or familiarization with new fields of research



how was the mass spec data analysed in this manuscript

- The mass spectrometry (MS) data in the manuscript was analyzed through the following detailed steps:
 - 1. Sample Preparation and Mass Spectrometry:
 - Desalted peptides were loaded onto a nano capillary and directly sprayed onto a Q-Exactive Plus Mass Spectrometer. The peptides were initially loaded in buffer A and eluted with buffer B using a specific gradient over time. The mass spectrometer operated in data-dependent acquisition mode, capturing one FT survey scan followed by ten HCD MS/MS scans per acquisition cycle.
 - Parameters included a mass range of 375 to 1400 m/z, resolution of 70,000, AGC target of 3E6, positive mode ionization voltage of 1.9 kV, and HCD fragmentation at a resolution of 17,500 with specific settings for AGC target, collision energy, injection time, and dynamic exclusion.

Data Processing:

- Raw data was processed using the MaxQuant computational platform (version 1.6.17.0) with standard settings for ITMS Ion trap data. The peak list was searched against the Uniprot Human database with specific mass deviation allowances for precursors and fragments. Modifications considered included cysteine carbamidomethylation as static and methionine oxidation and N-terminal acetylation as variable.
- The match-between-run option was enabled, and proteins were quantified using the label-free quantification (LFQ) algorithm, generating LFQ intensities.

3. Proteomic Data Analysis:

- The proteomic data was further processed using the RStudio package "DEP" for LFQbased differential analysis. The MaxQuant output table 'proteingroups.txt' served as the input, and data were prepared for differential analysis. Results were extracted and plotted using RStudio packages like ggplot2, dyplyr, and tidyverse. Significance was classified with a p-value of less than 0.05 and log2FoldChange thresholds for upregulated and downregulated proteins.
- Synaptosome fraction analyses included further analysis using SynGO, an interactive knowledge base using Gene Ontology (GO) annotations.

Applications of LLMs in Research Teaching

- Assistance in creating teaching outlines
- Assistance in creating teaching content
- Assistance in creating examination questions
- complete courses
- Replace in-person teaching with chatBot-based teaching

Sure! Learning R for data analysis in a molecular biology lab involves several key steps. Below is a structured guide to get you started, covering installation, basic usage, and specific techniques relevant to molecular biology.

Step 1: Install R and RStudio

1. Install R:

\$

- Go to the CRAN website.
- · Choose your operating system and follow the installation instructions.
- 2. Install RStudio (an integrated development environment for R):
 - Go to the RStudio website.
 - Download and install the free version for your operating system.

Step 2: Basic R Concepts and Syntax

- 1. R Console and Scripts:
 - You can run R commands directly in the console or write scripts (`.R` files) and execute them.
- 2. Basic Commands:



Applications of LLMs in Research Image interpretation and creation

ChatGPT 4 $\, \smallsetminus \,$



what tissue is this one?

The image you've uploaded shows a histological section of lung tissue, stained with hematoxylin and eosin (H&E). This common staining technique highlights the different components of the tissue, where the pink areas represent the cytoplasm and other extracellular matrix, and darker purple-blue regions indicate nuclei.

In this particular section, you can see structures that are characteristic of lung tissue, including bronchioles lined with epithelial cells and surrounded by supportive connective tissue. The large air-filled spaces are likely alveoli, the tiny sacs where gas exchange occurs. The appearance of the tissue suggests it could be from a region of the lung where both respiratory bronchioles and alveolar ducts/sacs are visible, indicative of a lower respiratory tract section.

Applications of LLMs in Research

Image interpretation and creation



can you create a scientific, schematic image of the respiratory tract. black white. 2D

Benefits of LLMs in Research

- Efficiency and time-saving
- Interactive access to a vast knowledge base, like talking to an expert
- lowers the barriers to familiarizing yourself with a new field or expanding your own expertise
- Improved accessibility for non-native English speakers
- Consistency and standardization of outputs
- Relatively unbiased assessment of knowledge
- Enhanced creativity and idea generation (not sure I agree, chatCPT)

The Perfect Wingman



The scientific process

Assistance or complete takeover by LLM



Challenges and Risks

Accuracy of Al-generated content

- Potential for errors and misinterpretation
- Transparency with respect to training data
- Moderation
- Hallucination



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😌 GWDG LLM Service – Generative Ai for Science – News		🙀 Chat Ai	
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Note: The chatbot is prone to hallucination and its responses should not be con accurate. Data Privacy and Imprint.	nsidered ×	Ask me	
Does Drosophila MOF acetylate the insulin receptor?			
A very specific question! According to the literature, the answer is yes, Drosophila MOF (Male-specific I humans) has been shown to acetviate the insulin receptor in Drosophila metar	ethal 3, MSL3 in		+ \$
MOF is a histone acetyltransferase that is known to play a role in various celluk chromatin remodeling and gene regulation. In the context of insulin signaling, I acetylate the insulin receptor (InR) in Drosophila, leading to increased insulin a uptake.	ar processes, including MOF has been found to signaling and glucose		
Studies have demonstrated that MOF-mediated acetylation of InR enhances it promoting the phosphorylation of downstream targets, such as Akt, and ultima glucose uptake in Drosophila cells.	s tyrosine kinase activity, ately leading to increased		
It's worth noting that while this specific interaction has been characterized in I MOF in insulin signaling and receptor acetylation is still being explored in other mammals.	Drosophila, the role of r organisms, including		
Would you like me to provide more information on this topic or help with some	thing else?		
please provide references			
Here are some references that support the statement that Drosophila MOF active receptor:	etylates the insulin		
 Xu et al. (2014): "MOF regulates insulin receptor mRNA translation and glu Drosophila" [1] 	cose metabolism in		
In this study, the authors show that MOF binds to the insulin receptor (InR) mR translation. They also demonstrate that MOF acetylates InR, leading to increas glucose uptake in Drosophila cells.	NA and regulates its ed insulin signaling and		
 Li et al. (2015): "MOF acetylates the insulin receptor and enhances insulin [2] 	signaling in Drosophila"	Model ⑦ Meta LLaMA 3 70B Instruct	~
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Challenges and Risks

Intellectual property concerns

- Originality and authorship issues
- Plagiarism, eg:
 - unintentional plagiarism in academic writing
 - journal article retraction due to AI-assisted plagiarism
 - grant proposal plagiarism detected by funding agency



✓ Bildrechte: picture alliance / SZ Photo | Florian Peljak

10.03.2024, 09:36 Uhr

🞧 Audiobeitrag

> Netzwelt > Zu gut, um menschlich zu sein? TUM lehnt Bewerber wegen KI ab

Zu gut, um menschlich zu sein? TUM lehnt Bewerber wegen KI ab

Ein Mann, der sich für einen Masterstudiengang an der Technischen Universität München beworben hatte, wurde wegen der Nutzung von ChatGPT beim Bewerbungsessay abgelehnt. Ein Gericht hat das nun bestätigt. Doch ist ein solches Vorgehen noch zeitgemäß?

Challenges and Risks Ethical dilemmas

- Bias in AI-generated outputs
- Privacy and data security concerns

https://www.wired.com/story/how-to-stop-your-data-from-being-used-to-train-ai/#:~:text=If you have an account,turn off Chat History & Training.

MATT BURGESS REECE ROGERS SECURITY APR 10, 2024 7:30 AM

How to Stop Your Data From Being Used to Train Al

Some companies let you opt out of allowing your content to be used for generative AI. Here's how to take back (at least a little) control from ChatGPT, Google's Gemini, and more.



Impact on Responsible Research Practices

Ethical guidelines for Al use in research

- Transparency and disclosure
- Accountability and oversight

Impact on Responsible Research Practices

(Current) best practices for integrating LLMs

- Critical evaluation of AI outputs
- Ensuring human oversight and intervention

Impact on Responsible Research Practices

Mitigating negative outcomes

• Strategies to prevent misuse

DFG guidelines Sept 2023

https://www.dfg.de/resource/blob/289676/89c03e7a7a8a024093602995974832f9/230921-statementexecutive-committee-ki-ai-data.pdf

- In view of its considerable opportunities and development potential, the use of generative models in the context of research work should by no means be ruled out.
- When making their results publicly available, researchers should, in the spirit of research integrity, **disclose** whether or not they have used generative models, and if so, which ones, for what purpose and to what extent.
- In decision-making processes, the use of generative models in/for proposals submitted to the DFG is currently assessed to be neither positive nor negative.
- The use of generative models in the preparation of reviews is inadmissible due to the confidentiality of the assessment process. Documents provided for review are confidential and in particular may not be used as input for generative models.

nature > editorials > article

EDITORIAL 24 January 2023

Tools such as ChatGPT threaten transparent science; here are our ground rules for their use

As researchers dive into the brave new world of advanced AI chatbots, publishers need to acknowledge their legitimate uses and lay down clear guidelines to avoid abuse.

Springer Nature journals principles

https://www.nature.com/articles/d41586-023-00191-1

- First, no LLM tool will be accepted as a credited author on a research paper. That is because any attribution of authorship carries with it accountability for the work, and AI tools cannot take such responsibility.
- Second, researchers using LLM tools should document this use in the methods or acknowledgements sections. If a paper does not include these sections, the introduction or another appropriate section can be used to document the use of the LLM.

Other concerns

- Dependence and Complacency
 - Decline in critical thinking and analytical skill
 - Increased use of AI could result in complacency, where researchers might trust AI outputs without adequate validation
- Quality and Reliability of Outputs: Propagation of Errors: Training -> Model -> Output -> Training
- Impact on Collaboration: LLMs can reduce opportunities for collaboration and discussion among researchers, which are vital for innovation and the cross-pollination of ideas
- Changes in Research Dynamics: The integration of LLMs might shift the focus from collaborative research to more individual-centric approaches, as AI tools can handle many tasks that traditionally required teamwork

Discussion and Q&A

Conclusion

- Recap of key points discussed
- Future outlook on AI and ethics in research
- Final thoughts and closing remarks